

Resource Summary Report

Generated by [kravitz2](#) on Aug 1, 2026

pFind

RRID:SCR_003011

Type: Tool

Proper Citation

pFind (RRID:SCR_003011)

Resource Information

URL: <http://pfind.ict.ac.cn/software/pFind/index.html>

Proper Citation: pFind (RRID:SCR_003011)

Description: A search engine system for automated peptide and protein identification from tandem mass spectra.

Resource Type: software resource

Defining Citation: [PMID:17702057](#)

Keywords: mass spectrometry, proteomics

Resource Name: pFind

Resource ID: SCR_003011

Alternate IDs: OMICS_02467

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260725T190536+0000

Ratings and Alerts

No rating or validation information has been found for pFind.

No alerts have been found for pFind.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 118 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Sellés-Baiget S, et al. (2025) Catalytic and noncatalytic functions of DNA polymerase γ in translesion DNA synthesis. *Nature structural & molecular biology*, 32(2), 300.

Zhao Q, et al. (2025) Nonenzymatic lysine D-lactylation induced by glyoxalase II substrate SLG dampens inflammatory immune responses. *Cell research*, 35(2), 97.

Gou J, et al. (2025) O-GlcNAcylated FTO promotes m6A modification of SOX4 to enhance MDS/AML cell proliferation. *Cell communication and signaling : CCS*, 23(1), 43.

Tian C, et al. (2025) Proteome-wide ligandability maps of drugs with diverse cysteine-reactive chemotypes. *Nature communications*, 16(1), 4863.

Ran Z, et al. (2025) Deciphering the MHC immunopeptidome of human cancers with Ligand.MHC atlas. *Briefings in bioinformatics*, 26(4).

Gu C, et al. (2025) Proteogenomic Reassessment Provides Novel Insight into the Life Cycle of *Tetrahymena thermophila*. *Molecular & cellular proteomics : MCP*, 24(11), 101081.

de-Dios T, et al. (2025) Bone Adhered Sediments as a Source of Target and Environmental DNA and Proteins. *Molecular biology and evolution*, 42(9).

Yu J, et al. (2025) In Vivo Ribosome-Amplified MetaBOLism, RAMBO, Effect Observed by Real Time Pulse Chase, RTPC, NMR Spectroscopy. *Biochemistry*, 64(12), 2660.

Zhu S, et al. (2025) Unraveling the Central Role of Global Regulator PprI in *Deinococcus radiodurans* Through Label-Free Quantitative Proteomics. *Proteomes*, 13(2).

He H, et al. (2025) Inhibition Peroxiredoxin-2 by Capsaicin Ameliorates Rheumatoid Arthritis via ROS-Mediated Apoptosis in Fibroblast-Like Synoviocytes. *MedComm*, 6(6), e70209.

Song Y, et al. (2025) Identification of Unknown Biological Toxin Proteins Using Mass Spectrometry: A Case Study on De Novo Sequencing of Ricin. *Toxins*, 17(11).

Li L, et al. (2025) Spatiotemporal single-cell architecture of gene expression in the *Caenorhabditis elegans* germ cells. *Cell discovery*, 11(1), 26.

Zhu TY, et al. (2025) Genetically encoding γ -N-methacryllsine into proteins in live cells. *Nature communications*, 16(1), 2623.

Fan L, et al. (2025) CICADA: a circRNA effort toward the ghost proteome. *Nucleic acids research*, 53(1).

Xiao C, et al. (2025) Oncogenic roles of young human de novo genes and their potential as neoantigens in cancer immunotherapy. *Cell genomics*, 5(9), 100928.

Wang Y, et al. (2025) Cytoplasmic TRIM24 promotes colorectal cancer cell proliferation by activating Wnt/ β -catenin signaling. *Nature communications*, 16(1), 8598.

Duong VA, et al. (2025) Metaproteomic Analysis to Assess the Impact of Storage Media on Human Gut Microbiome in Fecal Samples. *Proteomics*, 25(19), 39.

Wang C, et al. (2025) MCM7 promotes liver fibrosis by transcriptionally regulating IL11 via the SHCBP1-RACGAP1-STAT3 axis. *Cell death & disease*, 16(1), 608.

Ou Q, et al. (2025) Mesenchymal stromal cells induce neutrophil aggregation and extracellular vesicle storms for systemic lupus erythematosus. *Signal transduction and targeted therapy*, 10(1), 344.

Huang RH, et al. (2025) BPA: a BERT-based priority annotation strategy for assessing the rationality of aquatic algal protein sequences. *Briefings in bioinformatics*, 26(4).